RAW SEQUENCE LISTING

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Application Serial Number: 10/625, 204

Source: JFWO

Date Processed by STIC: 06/14/ 2005

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RAW SEQUENCE LISTING   DATE: 06/14/2005
PATENT APPLICATION: US/10/625,204   TIME: 14:02:14

Input Set : **A:\89DIV1.ST25.txt**
Output Set: **N:\CRF4\06142005\J625204.raw**

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 3 <110> APPLICANT: Figdor, Carl Gustav
 4       Geijtenbeek, Teunis Bernard Herman
 5       Van Kooyk, Yvette
 6       Torensma, Ruurd
 8 <120> TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING DENDRITIC CELL-T CELL
 9       INTERACTION
11 <130> FILE REFERENCE: 89 DIV
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C--> 13 **<140> CURRENT APPLICATION NUMBER: US/10/625,204**
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14 <141> CURRENT FILING DATE: 2003-07-23
16 <150> PRIOR APPLICATION NUMBER: 09/719,961
17 <151> PRIOR FILING DATE: 2001-09-24
19 <150> PRIOR APPLICATION NUMBER: PCT/NL00/00253
20 <151> PRIOR FILING DATE: 2000-04-19
22 <150> PRIOR APPLICATION NUMBER: US 60/176,924
23 <151> PRIOR FILING DATE: 2000-01-20
25 <150> PRIOR APPLICATION NUMBER: EP 99201204.7
26 <151> PRIOR FILING DATE: 1999-04-19
28 <160> NUMBER OF SEQ ID NOS: 2
30 <170> SOFTWARE: PatentIn version 3.2
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1215
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (1)..(1215)
42 <400> SEQUENCE: 1
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45 1               5                   10                  15
47 gag gaa cag ctg aga ggc ctt gga ttc cga cag act cga gga tac aag          96
48 Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys
49              20                  25                  30
51 agc tta gca ggg tgt ctt ggc cat ggt ccc ctg gtg ctg caa ctc ctc         144
52 Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu
53          35                  40                  45
55 tcc ttc acg ctc ttg gct ggg ctc ctt gtc caa gtg tcc aag gtc ccc         192
56 Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro
57      50                  55                  60
59 agc tcc ata agt cag gaa caa tcc agg caa gac gcg atc tac cag aac         240
60 Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn
61 65                  70                  75                  80
63 ctg acc cag ctt aaa gct gca gtg ggt gag ctc tca gag aaa tcc aag         288
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 64 Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys
 65             85              90              95
 67 ctg cag gag atc tac cag gag ctg acc cag ctg aag gct gca gtg ggt    336
 68 Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly
 69             100             105             110
 71 gag ctt cca gag aaa tct aag ctg cag gag atc tac cag gag ctg acc    384
 72 Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
 73         115             120             125
 75 cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag ctg cag    432
 76 Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
 77     130             135             140
 79 gag atc tac cag gag ctg acc tgg ctg aag gct gca gtg ggt gag ctt    480
 80 Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu
 81 145             150             155             160
 83 cca gag aaa tct aag atg cag gag atc tac cag gag ctg act cgg ctg    528
 84 Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
 85             165             170             175
 87 aag gct gca gtg ggt gag ctt cca gag aaa tct aag cag cag gag atc    576
 88 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile
 89         180             185             190
 91 tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ctt cca gag    624
 92 Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
 93         195             200             205
 95 aaa tct aag cag cag gag atc tac cag gag ctg acc cgg ctg aag gct    672
 96 Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala
 97     210             215             220
 99 gca gtg ggt gag ctt cca gag aaa tct aag cag cag gag atc tac cag    720
100 Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln
101 225             230             235             240
103 gag ctg acc cag ctg aag gct gca gtg gaa cgc ctg tgc cac ccc tgt    768
104 Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys
105             245             250             255
107 ccc tgg gaa tgg aca ttc ttc caa gga aac tgt tac ttc atg tct aac    816
108 Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn
109             260             265             270
111 tcc cag cgg aac tgg cac gac tcc atc acc gcc tgc aaa gaa gtg ggg    864
112 Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly
113         275             280             285
115 gcc cag ctc gtc gta atc aaa agt gct gag gag cag aac ttc cta cag    912
116 Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln
117     290             295             300
119 ctg cag tct tcc aga agt aac cgc ttc acc tgg atg gga ctt tca gat    960
120 Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp
121 305             310             315             320
123 cta aat cag gaa ggc acg tgg caa tgg gtg gac ggc tca cct ctg ttg   1008
124 Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu
125             325             330             335
127 ccc agc ttc aag cag tat tgg aac aga gga gag ccc aac aac gtt ggg   1056
128 Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly
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129              340              345              350
131 gag gaa gac tgc gcg gaa ttt agt ggc aat ggc tgg aac gac gac aaa    1104
132 Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys
133         355              360              365
135 tgt aat ctt gcc aaa ttc tgg atc tgc aaa aag tcc gca gcc tcc tgc    1152
136 Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys
137      370              375              380
139 tcc agg gat gaa gaa cag ttt ctt tct cca gcc cct gcc acc cca aac    1200
140 Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn
141 385              390              395              400
143 ccc cct cct gcg tag                                                 1215
144 Pro Pro Pro Ala
148 <210> SEQ ID NO: 2
149 <211> LENGTH: 404
150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
153 <400> SEQUENCE: 2
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156 1             5             10              15
159 Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys
160          20              25              30
163 Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu
164          35              40              45
167 Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro
168      50              55              60
171 Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn
172 65              70              75              80
175 Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys
176              85              90              95
179 Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly
180          100             105             110
183 Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
184          115             120             125
187 Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
188      130             135             140
191 Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu
192 145             150             155             160
195 Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
196              165             170             175
199 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile
200              180             185             190
203 Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
204          195             200             205
207 Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala
208      210             215             220
211 Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln
212 225             230             235             240
215 Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys
216              245             250             255
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219 Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn
220             260             265             270
223 Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly
224         275             280             285
227 Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln
228     290             295             300
231 Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp
232 305             310             315             320
235 Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu
236             325             330             335
239 Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly
240         340             345             350
243 Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys
244         355             360             365
247 Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys
248     370             375             380
251 Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn
252 385             390             395             400
255 Pro Pro Pro Ala
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VERIFICATION SUMMARY   DATE: 06/14/2005
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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number